



OIPE

RAW SEQUENCE LISTING

DATE: 03/19/2002

PATENT APPLICATION: US/10/084,700

TIME: 14:38:45

Input Set : A:\438d1.app

Output Set: N:\CRF3\03192002\J084700.raw

4 <110> APPLICANT: Seeley, Todd
 6 <120> TITLE OF INVENTION: huBUB3 GENE INVOLVED IN HUMAN CANCERS
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 12 <141> CURRENT FILING DATE: 2002-02-27
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 26 ctccctccgtg aagttcagcc ccaacacctc ccagttcctg cttgtctcct cctgggacac 180
 27 gtccgtgcgt ctctacgatg tgccggccaa ctccatgcgg ctcaagtacc agcacaccgg 240
 28 cgccgtcctg gactgcgcct tctacgatcc aacgcattgcc tggagtggag gactagatca 300
 29 tcaattgaaa atgcatgatt tgaacactga tcaagaaaat cttgttggga cccatgatgc 360
 30 ccctatcaga tgtgttgaat actgtccaga agtgaatgtg atggtcactg gaagttggga 420
 31 tcagacagtt aaactgtggg atcccagaac tccttgtaat gctgggacct tctctcagcc 480
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 33 cagagtgttg gtgtgggact tacggaacat gggttacgtg cagcagcgca gggagtccag 600
 34 cctgaaatac cagactcgct gcatacgagc gtttccaaac aagcagggtt atgtattaag 660
 35 ctctattgaa ggccgagtg cagttgagta tttggacca agccctgagg tacagaagaa 720
 36 gaagtatgcc ttcaaagtgc acagactaaa agaaaataat attgagcaga tttaccagtt 780
 37 caatgccatt tcttttcaca atatccacaa tacatttgcc acaggtgggt ctgatggctt 840
 38 tgtaaatatt tgggatccat ttaacaaaaa gcgactgtgc caattccatc ggtacccccc 900
 39 gagcatcgca tcacttgctt tcagtaatga tgggactacg cttgcaatag cgtcatcata 960
 40 tatgtatgaa atggatgaca cagaacatcc tgaagatggt atcttcattc gccaaagtgc 1020
 41 agatgcagaa acaaaaccca agtcaccatg tacttgacaa gatttcattt acttaagtgc 1080
 42 catgttgatg ataataaaac aattcgtact ccccaatggt ggatttatta ctattaaaga 1140
 43 aaccagggaa aatattaatt ttaatatatt aacaacctga aaataatgga aaagagggtt 1200
 44 ttgaattttt ttttttaaat aaacaccttc ttaagtgcatt gagatgggtt gatgggttgc 1260
 45 tgcattaaaag gtattttgggc aaacaaaatt ggagggcaag tgactgcagt tttgagaatc 1320
 46 agttttgacc ttgatgattt tttgtttcca ctgtggaaat aaatgtttgt aaataagtgt 1380
 47 aataaaaaatc cttttgcatt ctttctggac cttaaatggt agaggaaaag gctcgtgagc 1440
 48 cattttgtttc ttttgctggt tatagttgct aattctaaag ctgcttcaga ctgcttcatt 1500
 49 aggaggttaa tctacaatta aacaatattt cctcttgccc gtccattatt ttctgaagca 1560
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57 gaatgagatt catttcaatg taatgcacta aagcagaaca cgaacttagc ttggcctatt 2040
58 ctaggtagtt ccaaatagta tttttgttgt caaactttaa aatttatatt aatttgcaaa 2100
59 tgtatgtctc tgagtaggac ttggaccttt cctgagattt attttatccg tgatgtattt 2160
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78 20 25 30
79 Ser Ser Trp Asp Thr Ser Val Arg Leu Tyr Asp Val Pro Ala Asn Ser
80 35 40 45
81 Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
82 50 55 60
83 Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys
84 65 70 75 80
85 Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr His Asp
86 85 90 95
87 Ala Pro Ile Arg Cys Val Glu Tyr Cys Pro Glu Val Asn Val Met Val
88 100 105 110
89 Thr Gly Ser Trp Asp Gln Thr Val Lys Leu Trp Asp Pro Arg Thr Pro
90 115 120 125
91 Cys Asn Ala Gly Thr Phe Ser Gln Pro Glu Lys Val Tyr Thr Leu Ser
92 130 135 140
93 Val Ser Gly Asp Arg Leu Ile Val Gly Thr Ala Gly Arg Arg Val Leu
94 145 150 155 160
95 Val Trp Asp Leu Arg Asn Met Gly Tyr Val Gln Gln Arg Arg Glu Ser
96 165 170 175
97 Ser Leu Lys Tyr Gln Thr Arg Cys Ile Arg Ala Phe Pro Asn Lys Gln
98 180 185 190
99 Gly Tyr Val Leu Ser Ser Ile Glu Gly Arg Val Ala Val Glu Tyr Leu
100 195 200 205
101 Asp Pro Ser Pro Glu Val Gln Lys Lys Lys Tyr Ala Phe Lys Cys His
102 210 215 220
103 Arg Leu Lys Glu Asn Asn Ile Glu Gln Ile Tyr Pro Val Asn Ala Ile
104 225 230 235 240
105 Ser Phe His Asn Ile His Asn Thr Phe Ala Thr Gly Gly Ser Asp Gly

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108		260		265		270	
109	His Arg Tyr Pro Thr Ser Ile Ala Ser Leu Ala Phe Ser Asn Asp Gly						
110		275		280		285	
111	Thr Thr Leu Ala Ile Ala Ser Ser Tyr Met Tyr Glu Met Asp Asp Thr						
112		290		295		300	
113	Glu His Pro Glu Asp Gly Ile Phe Ile Arg Gln Val Thr Asp Ala Glu						
114	305		310		315		320
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126	gatacataca	gtgggtagaa	gagaattttc	ctgagaataa	agaatacttg	ataactttac	180
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128	tcagttattg	tttaaaattt	gctgagtaca	acagtgcctt	ccatcaattt	tttgagtttc	300
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139	taaaacagaa	aatggatgaa	cttcataaga	agttgcatca	ggtgggtggg	acatcccatg	960
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155	caccattcca	caagcttcca	gtggagtcag	tgacatcttt	agaagataaa	gaaaatgtgg	1920
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159 gtgaggcaga gttgggcgtt gaggcttgca gactcacaga cactgacgct gccattgcag 2160
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162 aactttttatc tgggctttct aaaccagtga gttcctatcc aaatactttt gaatggcaat 2340
163 gtaaaccttc agccatcaag cccaagactg aatttcaatt gggttctaag ctgggtctatg 2400
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194 35 40 45
195 Leu Glu His Leu Met Lys Glu Phe Leu Asp Lys Lys Lys Tyr His Asn
196 50 55 60
197 Asp Pro Arg Phe Ile Ser Tyr Cys Leu Lys Phe Ala Glu Tyr Asn Ser
198 65 70 75 80
199 Asp Leu His Gln Phe Phe Glu Phe Leu Tyr Asn His Gly Ile Gly Thr
200 85 90 95
201 Leu Ser Ser Pro Leu Tyr Ile Ala Trp Ala Gly His Leu Glu Ala Gln
202 100 105 110
203 Gly Glu Leu Gln His Ala Ser Ala Val Leu Gln Arg Gly Ile Gln Asn
204 115 120 125
205 Gln Ala Glu Pro Arg Glu Phe Leu Gln Gln Gln Tyr Arg Leu Phe Gln
206 130 135 140
207 Thr Arg Leu Thr Glu Thr His Leu Pro Ala Gln Ala Arg Thr Ser Glu

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210          165          170          175
211 Asn Pro Gly Asn Asn Met Ala Cys Ile Ser Lys Asn Gln Gly Ser Glu
212          180          185          190
213 Leu Ser Gly Val Ile Ser Ser Ala Cys Asp Lys Glu Ser Asn Met Glu
214          195          200          205
215 Arg Arg Val Ile Thr Ile Ser Lys Ser Glu Tyr Ser Val His Ser Ser
216          210          215          220
217 Leu Ala Ser Lys Val Asp Val Glu Gln Val Val Met Tyr Cys Lys Glu
218 225          230          235          240
219 Lys Leu Ile Arg Gly Glu Ser Glu Phe Ser Phe Glu Glu Leu Arg Ala
220          245          250          255
221 Gln Lys Tyr Asn Gln Arg Arg Lys His Glu Gln Trp Val Asn Glu Asp
222          260          265          270
223 Arg His Tyr Met Lys Arg Lys Glu Ala Asn Ala Phe Glu Glu Gln Leu
224          275          280          285
225 Leu Lys Gln Lys Met Asp Glu Leu His Lys Lys Leu His Gln Val Val
226          290          295          300
227 Glu Thr Ser His Glu Asp Leu Pro Ala Ser Gln Glu Arg Ser Glu Val
228 305          310          315          320
229 Asn Pro Ala Arg Met Gly Pro Ser Val Gly Ser Gln Gln Glu Leu Arg
230          325          330          335
231 Ala Pro Cys Leu Pro Val Thr Tyr Gln Gln Thr Pro Val Asn Met Glu
232          340          345          350
233 Lys Asn Pro Arg Glu Ala Pro Pro Val Val Pro Pro Leu Ala Asn Ala
234          355          360          365
235 Ile Ser Ala Ala Leu Val Ser Pro Ala Thr Ser Gln Ser Ile Ala Pro
236          370          375          380
237 Pro Val Pro Leu Lys Ala Gln Thr Val Thr Asp Ser Met Phe Ala Val
238 385          390          395          400
239 Ala Ser Lys Asp Ala Gly Cys Val Asn Lys Ser Thr His Glu Phe Lys
240          405          410          415
241 Pro Gln Ser Gly Ala Glu Ile Lys Glu Gly Cys Glu Thr His Lys Val
242          420          425          430
243 Ala Asn Thr Ser Ser Phe His Thr Thr Pro Asn Thr Ser Leu Gly Met
244          435          440          445
245 Val Gln Ala Thr Pro Ser Lys Val Gln Pro Ser Pro Thr Val His Thr
246          450          455          460
247 Lys Glu Ala Leu Gly Phe Ile Met Asn Met Phe Gln Ala Pro Thr Leu
248 465          470          475          480
249 Pro Asp Ile Ser Asp Asp Lys Asp Glu Trp Gln Ser Leu Asp Gln Asn
250          485          490          495
251 Glu Asp Ala Phe Glu Ala Gln Phe Gln Lys Asn Val Arg Ser Ser Gly
252          500          505          510
253 Ala Trp Gly Val Asn Lys Ile Ile Ser Ser Leu Ser Ser Ala Phe His
254          515          520          525
255 Val Phe Glu Asp Gly Asn Lys Glu Asn Tyr Gly Leu Pro Gln Pro Lys
256          530          535          540

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